

59520-00003.ST25.txt
SEQUENCE LISTING

<110> Atgen Co., Ltd.

Kim, Jong-Sun

<120> Novel Peptides Conferring Environmental Stress Resistance And Fusion Proteins
Including Said Peptides

<130> 59520-00003

<160> 37

<170> PatentIn version 3.1

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<211> 45

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(45)

<223> Acidic tail amino acid sequence 96-140 of alpha-synuclein

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Lys Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly
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Ile Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met
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Pro Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
35 40 45

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<223> Acidic tail amino acid sequence 85-134 of beta-synuclein

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Lys Arg Glu Glu Phe Pro Thr Asp Leu Lys Pro Glu Glu Val Ala Gln
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Glu Ala Ala Glu Glu Pro Leu Ile Glu Pro Leu Met Glu Pro Glu Gly
 20 25 30

Glu Ser Tyr Glu Asp Pro Pro Gln Glu Glu Tyr Gln Glu Tyr Glu Pro
 35 40 45

Glu Ala
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<223> Acidic tail amino acid sequence 96-127 of gamma-synuclein

<400> 3

Ala Lys Glu Asp Leu Arg Asp Ser Ala Pro Gln Gln Glu Gly Val Ala
 1 5 10 15

Ser Lys Glu Lys Glu Glu Val Ala Glu Glu Ala Gln Ser Gly Gly Asp

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25 30

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<222> (1)..(32)

<223> Acidic tail amino acid sequence 96-127 of synoretin

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His Lys Glu Ala Leu Lys Gln Pro Val Pro Ser Gln Glu Asp Glu Ala
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<223> GST-Syn96-140 fusion protein

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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser Glu Ile Trp Met Lys Lys Asp Gln Leu Gly Lys Asn Glu Glu
 225 230 235 240

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Asn Glu Ala Tyr Glu Met Pro Ser Glu Glu Gly Tyr Gln Asp Tyr Glu
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Pro Glu Ala
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<210> 6

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 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser His Met Glu Gln Val Thr Asn Val Gly Gly Ala Val Val Thr
 225 230 235 240

Gly Val Thr Ala Val Ala Gln Lys Thr Val Glu Gly Ala Gly Ser Ile
 245 250 255

Ala Ala Ala Thr Gly Phe Val Lys Lys Asp Gln Leu Gly Lys Asn Glu
 260 265 270

Glu Gly Ala Pro Gln Glu Gly Ile Leu Glu Asp Met Pro Val Asp Pro
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Asp Asn Glu Ala Tyr Glu Met Pro Ser Glu Glu Gly Tyr Gln Asp Tyr
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Glu Pro Glu Ala
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<222> (1)..(367)

<223> GST-Syn1-140 fusion protein

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5

10

15

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 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220

Gly Ser Ala Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu
 225 230 235 240

Gly Val Val Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala
 245 250 255

Ala Gly Lys Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys
 260 265 270

Glu Gly Val Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu
 275 280 285

Gln Val Thr Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val
 290 295 300

Ala Gln Lys Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly
 305 310 315 320

Phe Val Lys Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln
 325 330 335

Glu Gly Ile Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr
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Glu Met Pro Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
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ggtgatgtta aattaacaca gtctatggcc atcatagctt atatagctga caagcacaac	240
atgttgggtg gttgtccaaa agagcgtgca gagatttcaa tgcttgaagg agcggttttg	300
gatattagat acggtgtttc gagaattgca tatagtaaag actttgaaac tctcaaagtt	360
gattttctta gcaagctacc tgaaatgctg aaaatgttcg aagatcgttt atgtcataaa	420

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 ggagccccac aggaaggaat tctggaagat atgcctgtgg atcctgacaa tgaggcttat 780
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 tggcgaacaa aaaagtttga attgggtttg gagtttccca atcttcctta ttatattgat 180
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gatattagat acggtgtttc gagaattgca tatagtaaag actttgaaac tctcaaagtt 360
gattttctta gcaagctacc tgaaatgctg aaaatgttcg aagatcgttt atgtcataaa 420
acatatthaa atggtgatca tgtaacccat cctgacttca tgttgtatga cgctcttgat 480
gttgtttat acatggaccc aatgtgcctg gatgcttcc caaaattagt ttgttttaaa 540
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1105

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aacctgaagc ctaag 75

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39

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<222> (1)..(5)

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<400> 36

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1 5

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<222> (1)..(10)

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<400> 37

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1 5 10